

Amendments to the Claims:

Following is a complete listing of the claims pending in the application, as amended:

1-14. (Canceled)

15. (New) A method in a computer system for displaying a graphical representation of expression levels of a plurality of splice variants of a gene in one or more samples, each of the plurality of splice variants of the gene having modules and exons, the method comprising:

identifying modules and exons for each splice variant of the gene, each module or exon representing a subsequence of the splice variant and having a length L_s ,

applying a mathematical function to the length L_s of each subsequence to obtain a scaled length L_s' of each subsequence for graphical representation,

determining a relative expression level for each module or exon by applying a mathematical algorithm to expression level data for exon-exon junction indicator polynucleotides, and

displaying a graphical representation wherein the modules or exons of the splice variants are aligned with corresponding modules or exons of other splice variants of the gene and wherein the representation indicates the relative expression levels of the modules and exons.

16. (New) The method of claim 15, wherein the exon and modules are a minimal set of non-overlapping exons and modules.

17. (New) The method of claim 16, wherein the modules include exons, introns, extended portions of exons, and extended portions of introns.

18. (New) The method of claim 15, wherein the exons and modules are constitutive.

19. (New) The method of claim 15, wherein the exons and modules are non-constitutive.

20. (New) The method of claim 15, wherein the mathematical function is a linear equation.

21. (New) The method of claim 15, wherein the mathematical function is a logarithmic equation.